Regional Operational Plan SF.2A.2013.17

Upper Cook Inlet Commercial Eastside Set Gillnet Chinook Salmon Sampling Study

by

Tony Eskelin

June 2013

Alaska Department of Fish and Game **Divisions of Sport Fish and Commercial Fisheries**

Symbols and Abbreviations

The following symbols and abbreviations, and others approved for the Système International d'Unités (SI), are used without definition in the following reports by the Divisions of Sport Fish and of Commercial Fisheries: Fishery Manuscripts, Fishery Data Series Reports, Fishery Management Reports, and Special Publications. All others, including deviations from definitions listed below, are noted in the text at first mention, as well as in the titles or footnotes of tables, and in figure or figure captions.

Weights and measures (metric)	
centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)	
cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature	
day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry	
all atomic symbols	
alternating current	AC
ampere	A
calorie	cal
direct current	DC
hertz	Hz
horsepower	hp
hydrogen ion activity (negative log of)	pH
parts per million	ppm
parts per thousand	ppt, ‰
volts	V
watts	W

General	
Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat. or long.
monetary symbols (U.S.)	\$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Mathematics, statistics	
all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	log_2, etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

REGIONAL OPERATIONAL PLAN SF.2A.2013.17

UPPER COOK INLET COMMERCIAL EASTSIDE SET GILLNET CHINOOK SALMON SAMPLING STUDY

by

Tony Eskelin

Alaska Department of Fish and Game, Division of Sport Fish, Soldotna

Alaska Department of Fish and Game
Division

June 2013

The Regional Operational Plan Series was established in 2012 to archive and provide public access to operational plans for fisheries projects of the Divisions of Commercial Fisheries and Sport Fish, as per joint-divisional Operational Planning Policy. Documents in this series are planning documents that may contain raw data, preliminary data analyses and results, and describe operational aspects of fisheries projects that may not actually be implemented. All documents in this series are subject to a technical review process and receive varying degrees of regional, divisional, and biometric approval, but do not generally receive editorial review. Results from the implementation of the operational plan described in this series may be subsequently finalized and published in a different department reporting series or in the formal literature. Please contact the author if you have any questions regarding the information provided in this plan. Regional Operational Plans are available on the Internet at: http://www.adfg.alaska.gov/sf/publications/

Tony Eskelin,
Alaska Department of Fish and Game, Sport Fish Division,
43961 K-Beach Rd, Ste. B
Soldotna, AK 99669

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SIGNATURE/TITLE PAGE

Project Title:	Upper Cook Inlet commercial eastside set gillnet Chinook salmon sampling study
Project leader(s):	Tony Eskelin
Division, Region, and Area	Division of Sport Fish, Region II, Soldotna
Project Nomenclature:	
Period Covered:	2013 Field Season
Field Dates:	June 25-August 15, 2013
Plan Type:	Category III

Approval

Title	Name	Date
Project Leader	Tony Eskelin	6/10/2013
Co-Project Leader	Andy Barclay	6/10/2013
Biometrician	Anton Antonovich	6/10/2013
Regional Research Supervisor	Jack Erickson	6/20/2013
Fish and Game Coordinator	James Hasbrouck	6/21/2013

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PURPOSE

This project will collect and analyze age, sex, length (ASL), and genetic tissue samples of Chinook salmon harvested in the Upper Cook Inlet (UCI) eastside set gillnet (ESSN) commercial fishery. Genetic samples are needed to estimate the relative proportions and the number of Chinook salmon harvested in the ESSN commercial fishery temporally and geographically by reporting group. Sport Fish Division (SF) is responsible for the collection of genetic tissue samples and ASL data. Tissue samples will be sent to the Division of Commercial Fisheries (CF), Gene Conservation Lab (GCL), which will be responsible for mixed stock analysis (MSA).

BACKGROUND

Chinook salmon are harvested in a variety of mixed stock fisheries in UCI. Recent low Chinook salmon runs have heightened concerns about stock-specific harvest of Chinook salmon in these fisheries. A Chinook salmon genetic baseline that includes representative populations in UCI is now available for mixed stock analysis applications in fisheries using genetic stock identification (GSI) (Barclay et. al 2012). Obtaining information about stock-specific harvest of Chinook salmon is needed to improve understanding of stock productivity, brood table development, and for setting and attaining escapement goals.

The ESSN commercial fishery harvests the majority of Chinook salmon in the UCI commercial fishery. The fishery has 6 statistical areas, and 3 sections (Figure 1), all of which compose the Upper Subdistrict. The most recent 10-yr (2003–2012) average ESSN Chinook salmon harvest is 10,605 fish; however, harvest has declined recently. The recent 5-yr average (2008–2012) Chinook salmon harvest is 5,467 fish (Shields and Dupuis 2012). Due to low Chinook salmon abundance in 2012, the ESSN fishery was only open for 7 fishing periods, and 584 Chinook salmon were reported in the harvest, the lowest documented harvest.

The ESSN Chinook salmon harvest has been sampled for ASL composition information since the early 1980's. Normally, one technician would rove between buying stations on regular period openings and opportunistically collect ASL samples. Beginning in 2010, genetic tissue samples were added to the collection effort. With only one technician assigned to collect samples, it was difficult to adequately sample all areas of the ESSN fishery during each tide or fishing period. Some areas were targeted for sampling because they were expected to have larger Chinook salmon harvests, while some areas with lower harvest were not effectively sampled.

A sufficient number of representative samples were collected in 2010 and 2011 to allow for MSA, but not in 2012 (See Appendix A for full details of 2010-2012 collections and MSA). For the 2010 and 2011 collections, tissues were subsampled post season in proportion to the harvest within each statistical area (Ninilchik, Cohoe, South K. Beach, North K. Beach, South Salamatof, and North Salamatof). The goal was to have 400 individuals selected per year. The final number collected and successfully analyzed by GCL was 373 and 343 samples in 2010 and 2011, respectively. There was no temporal or geographic stratification, only seasonal estimates for 5 reporting groups: Kenai River mainstem, Kasilof River mainstem, Kenai River tributaries, Northwest Cook Inlet, and Coastal Southern Kenai Peninsula. The stock composition estimates for 2010 and 2011 were similar. In both years the Kenai River mainstem reporting group had the greatest proportional contribution (0.644 in 2010; 0.723 in 2011) followed by the Kasilof River mainstem reporting group (0.331 in 2010, 0.267 in 2011). The combined proportional contribution of all other reporting groups did not exceed 0.024 in either year.

This project in 2013 will involve expanded sampling of the Chinook salmon harvest for ASL and GSI. A total of three technicians will be assigned to sample the ESSN Chinook salmon harvest. The additional samplers should allow for better coverage of the fishery during regular period openings and also allow for sampling of some fishing periods opened by emergency order.

OBJECTIVES

1. Estimate the proportion of Chinook salmon harvest in the UCI ESSN commercial fishery by reporting group for each temporal and geographic stratum for the 2013 season such that the estimated proportions are within 0.13 of the true values 90% of the time.
2. Estimate the harvest of Chinook salmon in the UCI ESSN commercial fishery by reporting group for each temporal and geographic stratum such that the estimates are within 28% of the true value 90% of the time.
3. Estimate the age composition of the Chinook salmon harvested by the ESSN fishery such that the estimates are within 0.10 of the true values 95% of the time.

SECONDARY OBJECTIVES

1. Collect tissue and scale samples from 30% of Chinook salmon harvested in the UCI ESSN commercial fishery.
2. Estimate the sex and length compositions of Chinook salmon harvested in the UCI ESSN commercial fishery.

METHODS

STUDY DESIGN

The ESSN commercial fishery is scheduled for regular period openings from 7:00 AM to 7:00 PM Mondays and Thursdays. The first scheduled regular period in the Kasilof section (statistical areas 244-21, 244-22, and 244-31) is Thursday, June 27. The first scheduled regular period in the Kenai and East Forelands sections (statistical areas 244-32, 244-41, and 244-42) is Monday, July 8. A minimum of 2 technicians will sample Kasilof section-only openings (prior to the opening of the Kenai section) and 3 technicians will sample fishing periods thereafter. In addition, up to 2 fishing periods per week are budgeted to be sampled if opened by emergency order. Which emergency openings to sample will be chosen from harvest rates and insight from commercial fishery managers based on likely scenarios of future openings. The fishery is scheduled to end August 15 with only regular period openings allowed after August 10.

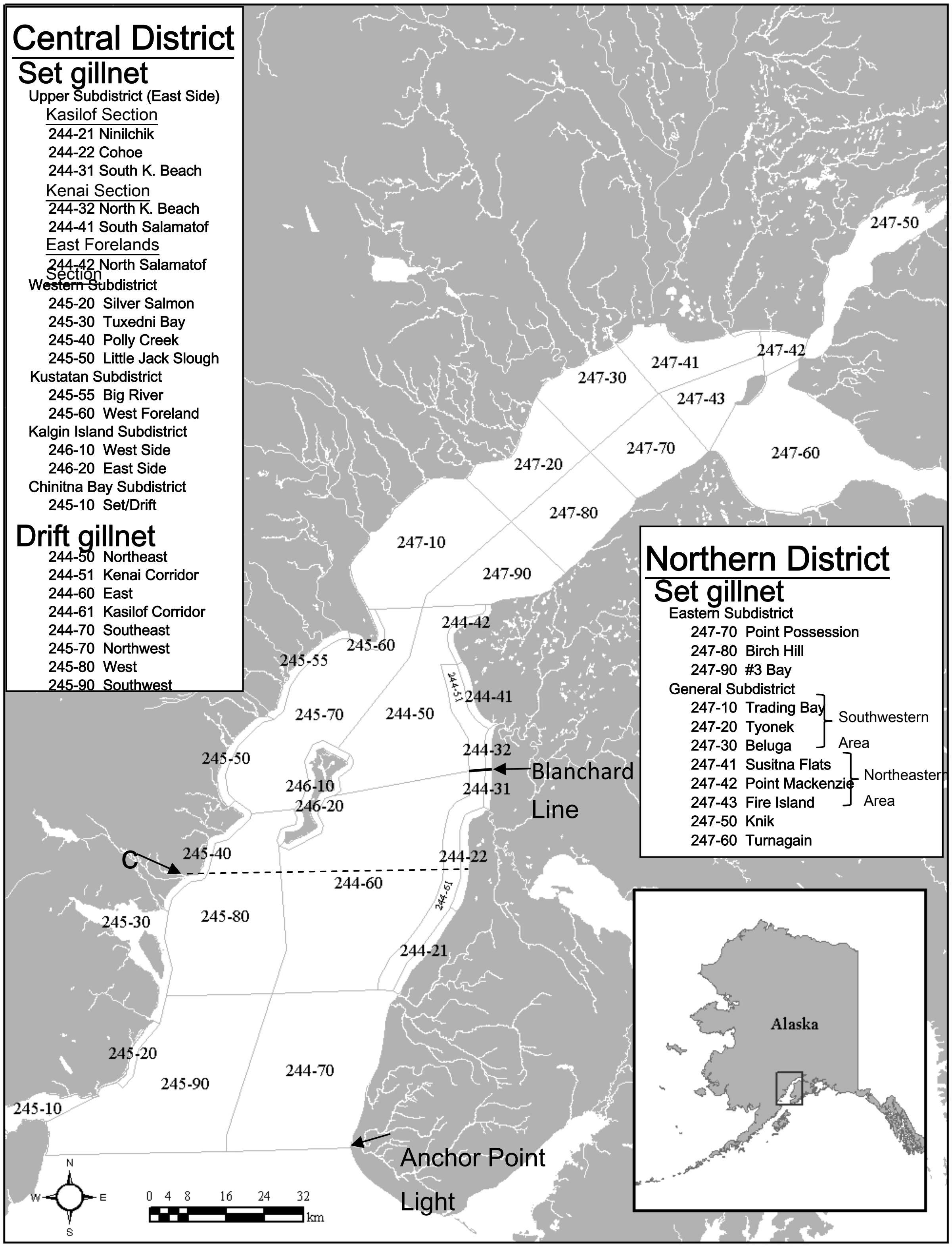

Figure 1.- Map of Upper Cook Inlet commercial fishing statistical areas.

The goal will be to sample as many Chinook salmon as possible while distributing sampling effort to allow for a representative sample of the harvest. Each technician will be assigned 1 of 3 areas to sample: 1) Ninilchik/Cohoe beaches, 2) K-beach (north and south), and 3) Salamatof beach (north and south) (Figure 1). There will likely be overlap in sampling areas among technicians and modifications to assigned areas may occur as the season progresses. Inseason analyses of the proportion of the Chinook salmon harvest sampled by beach will be conducted and modifications will be made to the sampling strategy as necessary. Technicians will begin sampling on the southern end of their sampling area after the first round of deliveries to each buying station. There will be approximately 25 locations where Chinook salmon are delivered to, which will be about 5 locations per statistical area. The project biologist will work with the CF sockeye salmon project biologist (Wendy Gist) and develop a list with contact information and a map showing locations to sample, which will be distributed to each technician. Technicians will be instructed to visit each buying station on their way north up the beach. There will be no set schedule for times to sample at each location. Schedules will depend on tides and fishing periods.

GEOGRAPHIC AND TEMPORAL STRATIFICATION WITH SAMPLE SIZES

Proposed temporal (prior to July 8, July 8-31, after July 31) and geographic (Kenai/East Foreland sections and Kasilof section) stratification was determined by management criteria and MSA results from 2010 and 2011 samples. Recent ESSN Chinook salmon harvests (2009–2011) were averaged to determine likely harvests for each stratum (Table 1).

Table 1.–Mean reported harvests of Chinook salmon in ESSN fishery 2009–2011.

Temporal Stratum	Kasilof Section	Kenai/East Forelands Sections
Prior to July 8	992	–
July 8-31	2,915	1,916
After July 31	377	522

A single technician sampling the fishery was able to sample 13% and 17% of the harvest in 2010 and 2011, respectively. After reviewing sample sizes for various sampling rates based on recent harvests, a sample rate of 30% was chosen as a goal for the 2013 harvest (Table 2).

Table 2.–Target collection sizes based on various hypothetical sampling rates and 2009–2011 mean ESSN Chinook salmon reported harvest.

	Kasilof Section				Kenai/East Forelands Sections			
	Sampling rate				Sampling rate			
Temporal Stratum	0.2	0.3	0.4	0.5	0.2	0.3	0.4	0.5
Prior to July 8	198	298	397	496	–	–	–	–
July 8–31	583	874	1,166	1457	383	575	766	958
After July 31	75	113	151	189	104	157	209	261

Samples must be collected to represent the harvest, which is seldom possible, so subsampling of collections is required postseason to ensure equal representation of the harvest. The mean selection rate of collections for 2010–2011 was 35%. The goal for 2013 is a 40% selection rate (Table 3).

Table 3.–Number of samples to analyze based on a selection rate of 0.35, 2009–2011 mean ESSN Chinook salmon reported harvest, and various harvest sampling rates.

	Kasilof Section				Kenai/East Forelands Sections			
	Sampling rate				Sampling rate			
Stratum	0.2	0.3	0.4	0.5	0.2	0.3	0.4	0.5
Prior to July 8	69	104	139	174	–	–	–	–
July 8-31	204	306	408	510	134	201	268	335
After July 31	26	40	53	66	37	55	73	91

In order to meet precision and accuracy objectives, a minimum of 100 samples per stratum are necessary for GSI. Based on a 30% harvest sampling rate, a 40% selection rate of subsamples, and 2009–2011 mean ESSN Chinook salmon harvests, we expect each stratum to achieve the 100 sampling minimum for all strata (Table 4).

Table 4.–Estimated sample sizes to analyze for GSI in 2013.

	Geographic Stratum	
Temporal Stratum	Kasilof Section	Kenai/East Forelands Sections
Prior to July 8	119	–
July 8–31	350	230
After July 31 (All)[a]	45	63
Total	514	292

[a] The After July 31 stratum will be a composite mixture of the Kasilof and Kenai/East Forelands sections.

Proof tests conducted by the GCL demonstrated that with a fishery mixture of 100 samples, we can estimate stock composition for the 3 reporting groups (Kenai mainstem, Kasilof mainstem, and Other CI) within 0.13 of the true values 90% of the time. These tests were conducted under the 'worst-case' scenario for stock proportions deemed possible in fishery mixtures of ESSN fishery – 0.47 for Kenai Mainstem, 0.47 for Kasilof Mainstem, and 0.06 for Other CI. With this precision of stock composition estimates we will be able to estimate the ESSN Chinook salmon harvest in each stratum within 28% of the true values 90% of the time.

The objective criterion (± 0.10 with 95% confidence level) for estimating the age composition of Chinook salmon harvested in the ESSN fishery should be achieved with approximately 170 scale samples. To arrive at this sample size we assumed 25% scale regeneration rate and the worst-case scenario for multinomial proportions (Thompson 1987). As we plan to collect substantially more samples in 2013 (approx. 800) we are likely to achieve higher precision for the age composition estimates.

DATA COLLECTION

All Chinook salmon sampled will be recorded by statistical area and will be sampled for age, sex, length, and genetic tissue. For genetic tissue collections a ½ inch piece from the tip of an axillary process fin will be removed from each fish and placed in a 2ml plastic vial (Nalgene, VWR Cat. # 66008-710) and completely covered with a Sigma Reagent Grade 95% Alcohol

(Sigma Cat. # R 8382) buffer solution such that the liquid to tissue ratio is approximately 3:1. Each plastic tube will be sequentially numbered and the vial number will be recorded in the field computer or on data sheets (Appendix A). All plastic vials will be stored at the Soldotna office until the end of the season when all tubes will be sent to the GCL for analysis. For age, 3 scales will be taken from the left side of the body of each sampled fish, at a point on a diagonal from the posterior insertion of the dorsal fin to the anterior insertion of the anal fin, 2 rows above the lateral line (Welander 1940), and placed on an adhesive-coated card. An impression is made of the scales on the card using a press under 25,000 PSI and the scale growth patterns are viewed with a 40x microfiche reader to determine freshwater and marine residence times. Sex will be determined using external visual cues. Mid-eye fork length (MEFL) will be measured to the nearest 5 mm.

LABORATORY ANALYSIS

Assaying genotypes

DNA extraction and genotyping will generally follow the methods described in detail in Barclay et al. (2012). Briefly, genomic DNA will be extracted from tissue samples using a DNeasy 96 Tissue Kit by QIAGEN (Valencia, CA). Fluidigm 192.24 Dynamic Arrays (http://www.fluidigm.com) will be used to screen 40 SNP markers; this differs from the methods of Barclay et al. (2012) where they used 96.96 Dynamic Arrays. The Dynamic Arrays will be read on a Fluidigm EP1 System or BioMark System after amplification and scored using Fluidigm SNP Genotyping Analysis software. Assays that fail to amplify on the Fluidigm system will be reanalyzed on the Applied Biosystems platform. The plates will be scanned on an Applied Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems' Sequence Detection Software version 2.2.

Genotypes produced on both platforms will be imported and archived in the Gene Conservation Laboratory (GCL) Oracle database, LOKI.

Laboratory Failure Rates and Quality Control

Overall failure rate will be calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. An individual genotype will be considered a failure when a locus for a fish cannot be satisfactorily scored.

Quality control (QC) measures will be used to identify laboratory errors and to determine the reproducibility of genotypes. In this process, 8 of every 96 fish (1 row per 96-well plate) will be reanalyzed for all markers by staff not involved with the original analysis. Laboratory errors found during the QC process will be corrected, and genotypes will be corrected in the database. Inconsistencies not attributable to laboratory error will be recorded, but original genotype scores will be retained in the database.

DATA REDUCTION

Technicians will return their genetic vial boxes, scale cards, field computers, and field data to the Soldotna office daily and will be responsible for ensuring the recorded data are legible and accurate. Paper forms will be available as a backup in the event the field computer fails. Age data are keypunched directly into master electronic data files after age is determined by scale reading. The project biologist will ensure all data are returned, are legible, and are entered correctly. Data maps for all of the information collected in this project are shown in Appendix

C. A final edited copy of all data files along with a data map will be sent to the Alaska Department of Fish and Game Research and Technical Services (RTS) for archiving.

DATA ANALYSIS

MIXED STOCK ANALYSIS

Estimates of Chinook salmon stock composition and harvest by reporting group will be stratified temporally and geographically. Reporting groups will be 1) Kenai River mainstem, 2) Kasilof River mainstem, and 3) all other Cook Inlet stocks. Temporal strata will be: 1) prior to July 8, 2) July 8-31, and 3) after July 31. Geographic strata will be 1) Kenai/East Forelands Sections and 2) Kasilof section.

The stock composition of the commercial ESSN fishery harvest for each stratum will be estimated using the software package BAYES (Pella and Masuda 2001). BAYES employs a Bayesian algorithm to estimate the most probable contribution of the baseline populations to explain the combination of genotypes in the mixture sample. The final analysis will consist of the results from 5 separate Monte Carlo Markov chains where each chain will begin with different initial values. A random number generator will be used to create the initial values which will sum to 1 over all reporting groups. The prior distribution in BAYES will be based upon the best available information for each mixture analysis. We believe the best available information for the prior to be the results of MSA of similar mixtures. For the 2013 ESSN mixtures, the best available information will be the stock proportions estimates from the analysis of the 2011 ESSN Chinook salmon samples. The sum of the prior parameters will equal one, thus minimizing the overall influence of the prior distribution. The chains will be run until convergence is reached (shrink factor < 1.2) for the 5 chains (Pella and Masuda 2001). The first half of each chain will be discarded in order to remove the influence of the initial values; the rest will be used to estimate the posterior distribution of stock composition proportions. The point estimates of stock composition and the variance of these estimates will be calculated from the mean and standard deviation of the posterior distributions.

HARVEST OF MAINSTEM-KENAI- AND KASILOF-ORIGIN CHINOOK SALMON

The number of Kenai mainstem-origin Chinook salmon ($\hat{H}^{Ke}$) harvested in the commercial ESSN fishery between the first opening in late June and August 15 will be estimated as:

$$\hat{H}^{Ke} = \sum_{i-1}^{T} \sum_{j=1}^{S} H_{i,j}\,\hat{p}_{i,j}^{Ke} \tag{1}$$

where

$\hat{p}_{i,j}^{Ke}$ = estimated proportion of ESSN harvest in time stratum *i* and geographic stratum *j* comprising Kenai mainstem-origin Chinook salmon. Obtained based on Bayesian mixed stock analysis as described in the previous section.

$H_{i,j}$ = ESSN Chinook salmon harvest in time stratum *i* and area stratum *j* obtained from fish ticket data.

T = number of time strata (prior to July 8, July 8-31, and after July 31)

S = number of geographic strata (Kenai and Kasilof sections)

$\mathrm{var}(\hat{H}^{Ke})$ will be estimated as:

$$\mathrm{var}(\hat{H}^{Ke}) = \sum_i \sum_j (H_{i,j})^2 \ \mathrm{var}(\hat{p}_{i,j}^{Ke}) \tag{2}$$

where $\mathrm{var}(\hat{p}_{i,j}^{Ke})$ will be available from the Bayesian mixed stock analysis (Pella and Masuda, 2001).

The number of Kasilof mainstem-origin Chinook salmon ($\hat{H}^{Ka}$) harvested in the commercial Eastside set net fishery and its variance will be estimated using equations (1) and (2) with the estimated proportion of Kasilof mainstem-origin Chinook salmon in time stratum *i* and area stratum *j* $\hat{p}_{i,j}^{Ka}$, substituted instead of $\hat{p}_{i,j}^{Ke}$.

AGE COMPOSITION OF CHINOOK SALMON IN ESSN HARVEST

The age proportions of Chinook salmon harvested in the commercial ESSN fishery by sampling stratum will be estimated as:

$$\hat{p}_{i,j}^{z} = \frac{n_{i,j}^{z}}{n_{i,j}} \tag{3}$$

where $\hat{p}_{i,j}^{z}$ is the estimated proportion of salmon of age category *z* from sampling stratum (*i*, *j*), $n_{i,j}^{z}$ equals the number of fish sampled from sampling stratum (*i*, *j*) that were classified as age category *z*, and $n_{i,j}$ equals the number of Chinook salmon sampled for age determination from sampling stratum (*i*, *j*).

The variance of $\hat{p}_{i,j}^{z}$ will be calculated by:

$$\mathrm{var}\left[\hat{p}_{i,j}^{z}\right] = \left(1 - \frac{n_{i,j}}{H_{i,j}}\right) \frac{\hat{p}_{i,j}^{z}\left(1 - \hat{p}_{i,j}^{z}\right)}{n_{i,j} - 1} \tag{4}$$

where $H_{i,j}$ is the number of Chinook salmon harvested in a sampling stratum (*i*, *j*).

The estimates of harvest by age categories in each sampling stratum will be calculated by:

$$\hat{H}_{i,j}^{z} = H_{i,j}\,\hat{p}_{i,j}^{z} \tag{5}$$

with its variance estimated as:

$$\mathrm{var}\left[\hat{H}_{i,j}^{z}\right] = H_{i,j}^{2} * \mathrm{var}\left[\hat{p}_{i,j}^{z}\right] \tag{6}$$

The total harvest by age category and its variance will then be estimated by summation:

$$\hat{H}^{z} = \sum_{i=1}^{T} \sum_{j=1}^{S} \hat{H}_{i.j}^{z} \qquad \text{var}\left[\hat{H}^{z}\right] = \sum_{i=1}^{T} \sum_{j=1}^{S} \text{var}\left[\hat{H}_{i,j}^{z}\right] \tag{7}$$

where: *T*=3, *S*=2 are the number of time and geographic strata respectively.

Finally, the total proportion of the ESSN harvest by age category and its variance will be estimated by:

$$\hat{p}^{z} = \frac{\hat{H}^{z}}{H} \qquad \text{var}\left[\hat{p}^{z}\right] = \frac{\text{var}\left[\hat{H}^{z}\right]}{H^{2}} \tag{8}$$

BUDGET SUMMARY

Proposed FY13 and FY14 Costs:

Line Item	Category	FY13 Budget ($K)	FY14 Budget ($K)
100	Personnel	4.6	69.7
200	Travel	---	---
300	Contractual	1.4	27.2
400	Commodities	0.5	7.7
500	Equipment	---	---
Total		6.5	104.6

Funded Personnel FY 13:

PCN	Name	Level	Funded Man Months
	Vacant	FWT II	0.23
114062	Fender, Shannon	FWT II	0.23
Total			0.46

Funded Personnel FY 14:

PCN	Name	Level	Funded Man Months
115244	Eskelin, Anthony	Fishery Biologist II	1.0
	Barclay, Andy	Fishery Biologist III (CF)	1.0
	Antonovich, Anton	Biometrician III	1.0
	Vacant	FWT II	1.5
	Vacant	FWT II	1.5
114062	Fender, Shannon	FWT II	1.5
Total			8.5

SCHEDULE AND DELIVERABLES

Date	Activity
Mid – late June 2013	Hiring and preseason training (Eskelin)
Late June – mid August 2013	ESSN Chinook salmon harvest sampling (3 FWT II)
August 25, 2013	Data edited and tissue collection transferred to GCL (Eskelin)
September 15, 2013	Scales aged (Gist)
October 15, 2013	ASL composition estimates (Eskelin)
November 4, 2013	Tissues analyzed by GCL and MSA results disseminated (Barclay)
November 25, 2013	Harvest estimates completed by temporal, geographic strata and reporting group. (Eskelin and Antonovich)
January 10, 2014	Memo detailing ESSN Chinook GSI results through 2013 (Eskelin and Barclay)
Spring, 2014	FDS Report draft out for review (Eskelin and Barclay)
Spring, 2014	FDS report published (Eskelin and Barclay)

RESPONSIBILITIES

PRINCIPAL INVESTIGATOR

Tony Eskelin, Project Leader, Fishery Biologist II:

The project leader is responsible for writing the operational plan. This position will serve as the project biologist and will be responsible for hiring and training personnel and supervision of data collection. The project biologist will be responsible for collating data and transferring tissue samples to Anchorage for GSI analysis and any associated data. This position will also ensure all data is in proper format and archived with RTS at the completion of the field season and will be primary author on any reporting.

CO PRINCIPAL INVESTIGATOR

Andy Barclay, Fishery Biologist III:

This position is the Gene Conservation Lab representative. This position is responsible for the analysis of tissue samples for GSI, providing estimates and individual sample assignments to the project biologist and biometrician. This position will be co-author on FDS reports.

CONSULTING BIOMETRICIAN

Anton Antonovich, Biometrician III:

Provides guidance on sampling design and data analysis. Prepares estimate of harvest of Chinook salmon by reporting group. Assists with preparation of operational plan and report.

SCALE AGER

Wendy Gist Fishery Biologist I:

Position will age scales and provide ages to project biologist.

SAMPLING CREW

Vacant, Fish and Wildlife Technician II, 24 June – 16 August.

Responsibilities of these positions include: crew lead of sampling crew, adhering to sampling schedule; sampling harvested Chinook salmon for ASL and tissue; recording data accurately; entering data into a computerized database in a timely manner.

Shannon Fender, Fish and Wildlife Technician II, 24 June – 16 August.
Vacant, Fish and Wildlife Technician II, July 1 – 16 August.

Responsibilities of these positions include: operating state of Alaska vehicles, adhering to sampling schedule; sampling harvested Chinook salmon for ASL and tissue; recording data accurately; entering data into a computerized database in a timely manner.

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APPENDIX A. MEMORANDUM DETAILING 2010-2012 ESSN CHINOOK SALMON COLLECTIONS AND MSA

Appendix A1.–Memorandum to Regnart and Swanton detailing 2010-2012 ESSN Chinook salmon collections and MSA.

MEMORANDUM

State of Alaska

Department of Fish and Game

Division of Commercial Fisheries

TO:	Jeff Regnart Division of Commercial Fisheries Director And Charles Swanton Sport Fish Division Director	DATE:	November 30, 2012
THROUGH:	William Templin Fisheries Scientist I	PHONE NO:	267-2290
FROM:	Andrew Barclay Fishery Biologist III	SUBJECT:	ESSN Chinook salmon MSA

From 2010 to 2012 genetic tissue samples were collected opportunistically from Chinook salmon harvested in the Upper Cook Inlet (UCI) Upper Subdistrict set gillnet fishery, commonly referred to as the East Side Set Net (ESSN) fishery. Tissue samples were collected from Chinook salmon during regular openings at receiving sites and occasionally from a fish processor the following day. The sampling goal for each fishing period was to sample as many Chinook salmon as possible during each tide from all areas of the ESSN fishery. Because there was only one dedicated person to collect these samples, some areas of the ESSN fishery could not be sampled during each tide. Additionally, some areas were targeted for sampling because they were expected to have larger Chinook salmon harvests, while some areas with lower harvests were not sampled. A total of 885, 1281, and 185 Chinook salmon genetic tissue samples were collected in 2010, 2011, and 2012, respectively.

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In 2012 the ESSN fishery was closed for much of the season to protect Chinook salmon returning to the Kenai River. In the fall of 2012, the Gene Conservation Laboratory was directed to proceed with analysis of the collected samples to determine the stock composition the ESSN during the three years. Based on discussions with biologists and biometricians from both Commercial Fisheries and Sport Fish divisions, the 2012 samples were excluded from the analysis because of the low sample size and restricted fishing periods from which they originated. The GCL generally does not release estimates that might have management or allocation implications until data are collected over a minimum of three years. However, due to the public interest in this question, the GCL has analyzed the 2010 and 2011 collections and the results are provided in this memo. These estimates should be viewed as preliminary until data from a more structured study plan from additional years are analyzed.

The current genetic baseline for UCI Chinook salmon contains a total of 66 individual collections representing 32 populations which have been analyzed for 40 single nucleotide polymorphism loci (Table 1; Figure 1). This baseline contains the same set of loci and collections as the baseline reported in Barclay et al. (2012) with the exception of two additional Kenai River populations (Grant Creek and Lower Kenai River mainstem). The updated baseline was used in the analysis of the ESSN fishery samples; however, Slikok Creek (Kenai River) was removed from the baseline because it is a very small population and it is genetically similar to Crooked Creek (Kasilof River). Initial tests of the baseline (which included Slikok Creek) for mixed-stock analysis (MSA) indicated that a large portion of Crooked Creek fish misallocated to Slikok Creek. Once Slikok Creek was excluded, MSA tests of the baseline indicated that adequate genetic differentiation existed among all the reporting groups and that they could be used with high confidence (at least 90% correct allocations in 100% proof tests; see methods in Barclay et al. 2010). These reporting groups include: 1) all UCI Chinook population North and West of the Kenai River; *NorthwestCI*, 2) Kenai River tributary populations (excluding Juneau Creek); *KenaiTrib*, 3) Kenai River mainstem populations including Juneau Creek; *KenaiMainstem*, 4) the Kasilof River mainstem population; *KasilofMainstem*, and 5) Anchor River, Ninilchik River, Deep Creek, and Crooked Creek; *CoastalSKenaiPen* (Table 1; Figure 1). Although Juneau Creek is a tributary of the Kenai River it was included in the Kenai River mainstem reporting group because it is genetically similar to Kenai River mainstem populations.

For the 2010 and 2011 collections, tissues were subsampled in proportion to the harvest within statistical areas of the Upper Subdistrict (Ninilchik, Cohoe, South K. Beach, North K. Beach, South Salamatof, and North Salamatof), with a goal of 400 individuals per year. Some tissue samples in 2010 and 2011 were collected at processors which received deliveries from multiple statistical areas. Because the specific statistical area of these samples was not identified, these samples were excluded from analysis. A total of 376 and 347 samples were selected for analysis from 2010 and 2011, respectively. Several samples from 2010 (3) and 2011 (5) were excluded from the analysis because they failed to genotype at more than 20% of loci screened (see methods in Barclay et al. 2012). These individuals were removed because the inclusion of individuals with poor quality DNA might introduce genotyping error and reduce the accuracy of the MSA. The final number of successfully analyzed samples was 373 and 342 samples in 2010 and 2011, respectively.

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The MSA program BAYES was used to estimate the proportions of the 5 reporting groups (stocks; Figure 1) contributing to each fishery sample. The analysis employed a similar the BAYES protocol reported in Barclay et al. (2010) for baseline evaluation tests, except that each fishery sample was analyzed for 5 chains with 40,000 iterations per chain. Estimates and 90% credibility intervals for each fishery sample were tabulated from the combined set of the second half of each chain (100,000 iterations).

The stock composition estimates for 2010 and 2011 were similar. In both years the Kenai River mainstem reporting group had the greatest contribution followed by the Kasilof River mainstem reporting group. The combined contribution of all other reporting groups in both years did not exceed 2.4% (Table 2; Figure 2).

Please let me know if you have any questions regarding this analysis.

Appendix A1.–Table 1. Tissue collections of Chinook salmon collected throughout Upper Cook Inlet including the year sampled, number of samples collected (N), the number of individuals analyzed from each collection included in the baseline and their assigned reporting group for the analysis of the East Side Set Net fishery collections. Unique population numbers represent all the analyzed collections that contribute to a single population.

Pop. No.	Reporting Group	Location	Year Collected	N	Analyzed
1	NorthwestCI	Straight Creek	2010	105	95
2		Chuitna River	2008	20	20
2			2009	122	122
3		Coal Creek	2009	42	42
3			2010	35	35
4		Middle Fork Chulitna River	2009	72	72
4			2010	97	97
5		Stephan Lake weir	2008	19	19
5		Prairie Creek	1995	52	52
5			2008	98	98
6		Chunilna Creek	2009	50	50
7		Montana Creek	2008	33	33
7			2009	155	155
7			2010	30	30
8		Deception Creek	2009	122	100
8		Willow Creek	2005	74	74
9		Moose Creek	1995	51	51
9		Deshka River weir	2005	200	200
10		Talachulitna River	1995	58	58
10			2008	74	72
10			2010	48	48
11		Sunflower Creek	2009	53	53
12		Little Susitna River	2009	3	3
12			2010	122	122
13		Moose Creek	1995	20	20
13			2008	33	33
13			2009	22	22
14		Ship Creek	2009	311	311
15		Chickaloon River	2008	2	2
15			2010	66	65

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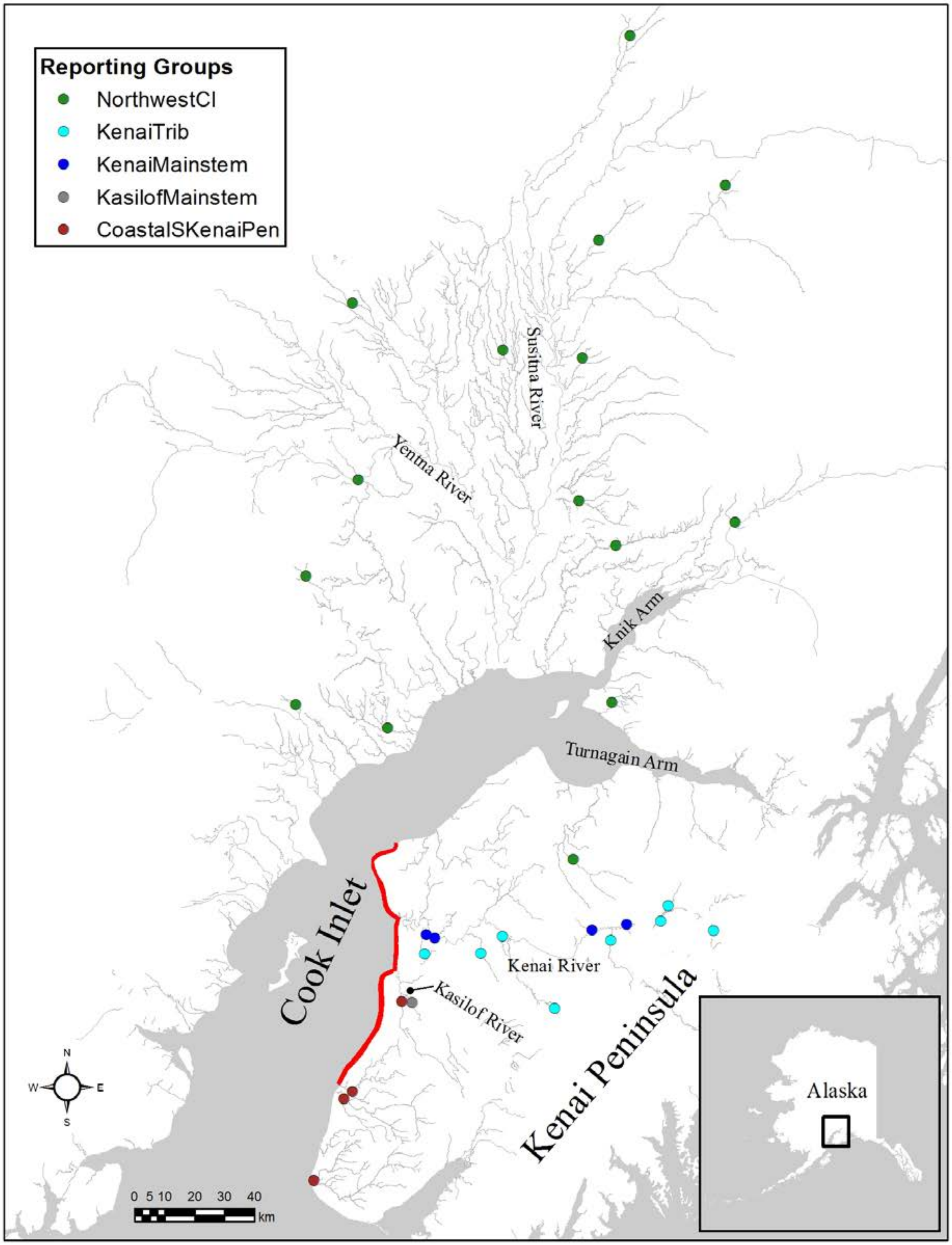
Appendix A1.–Table 1. Page 2 of 2.

Pop. No.	Reporting Group	Location	Year Collected	N	Analyzed
16	KenaiTrib	Grant Creek	2011	23	23
16			2012	32	32
17		Quartz Creek	2006	35	34
17			2008	34	34
17			2009	41	41
17		Dave's Creek	2007	8	8
17			2008	5	5
18		Crescent Creek	2006	165	165
19		Russian River	2005	24	24
19			2006	16	16
19			2007	84	83
19			2008	91	91
20		Benjamin Creek	2005	56	56
20			2006	150	150
21		Killey River	2005	68	68
21			2006	190	190
22		Funny River	2005	37	37
22			2006	183	183
23		Slikok Creek	2004	48	48
23			2005	100	95
23			2008	58	57
24	KenaiMainstem	Juneau Creek	2005	32	32
24			2006	100	91
24			2007	24	24
25		Upper Kenai River mainstem	2009	200	200
26		Middle Kenai River mainstem	2003	80	80
26			2004	39	39
26			2006	183	183
27		Lower Kenai River mainstem	2011	90	80
28	KasilofMainstem	Lower Kasilof River mainstem	2005	144	49
28		Middle Kasilof River mainstem	2005	273	273
29	CoastalSKenaiPen	Crooked Creek	1992	95	95
29			2005	212	212
30		Ninilchik River weir	2006	190	162
31		Deep Creek	2009	100	100
32		Anchor River weir	2006	200	200

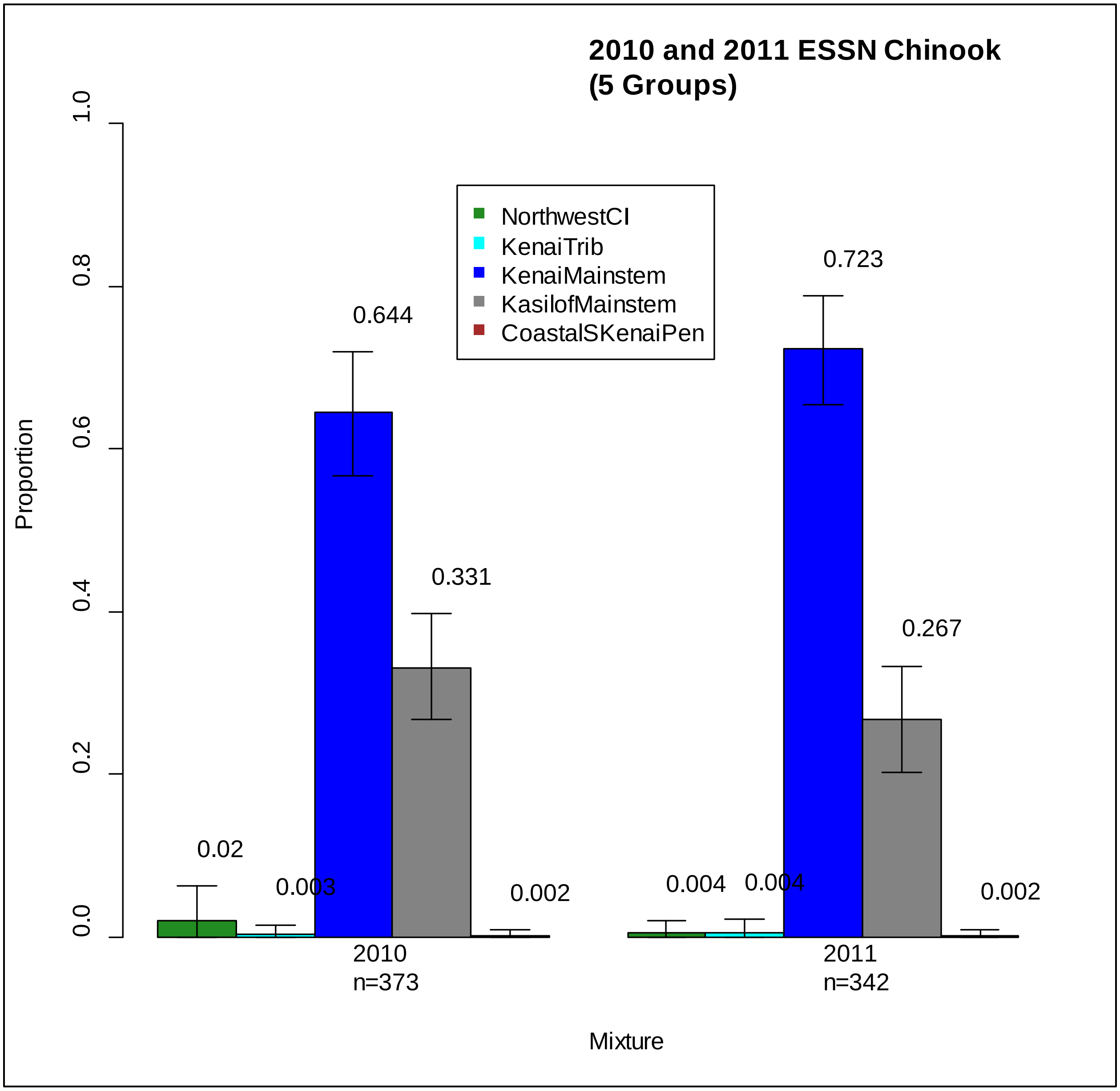
Appendix A1.–Table 2. Stock proportion estimates, standard deviation (SD), sample size (n), and lower (5%) and upper (95%) bounds of the 90% credibility interval for mixtures of Chinook salmon harvested in the east side set net fishery in 2010 and 2011.

	2010 (n= 373)				2011 (n=342)			
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NorthwestCI	0.020	0.022	0.000	0.063	0.004	0.007	0.000	0.019
KenaiTrib	0.003	0.006	0.000	0.015	0.004	0.008	0.000	0.021
KenaiMainstem	0.644	0.046	0.566	0.719	0.723	0.041	0.654	0.788
KasilofMainstem	0.331	0.040	0.267	0.398	0.267	0.040	0.203	0.333
CoastalSKenaiPen	0.002	0.004	0.000	0.009	0.002	0.004	0.000	0.009

Appendix A1.–Figure 1. Sampling locations (dots) for Chinook salmon used to compile a genetic baseline for Upper Cook Inlet. East Side Set Net fishery area is highlighted in red. Colors for each reporting group are indicated in the legend.



Appendix A1.–Figure 2. Stock proportion estimates for Chinook salmon harvested in the East Side Set Net (ESSN) fishery of Upper Cook Inlet in 2010 and 2011. Numbers above the bars are the mean estimates, n is the sample size of the fishery sample for each year, and whiskers indicate the upper and lower bounds of the 90% credibility interval.



APPENDIX B. PRELIMINARY ESSN CHINOOK SALMON SAMPLING SCHEDULE

Appendix B1.–Preliminary ESSN Chinook salmon sampling schedule.

Sunday	Monday	Tuesday	Wednesday	Thursday	Friday	Saturday
16-Jun	**17-Jun**	**18-Jun**	**19-Jun**	**20-Jun**	**21-Jun**	**22-Jun**
23-Jun	**24-Jun**	**25-Jun**	**26-Jun**	**27-Jun**	**28-Jun**	**29-Jun**
	Training			**Regular Period Kasilof section**		
30-Jun	**1-Jul**	**2-Jul**	**3-Jul**	**4-Jul**	**5-Jul**	**6-Jul**
	Regular Period Kasilof section			**Regular Period Kasilof section**		
7-Jul	**8-Jul**	**9-Jul**	**10-Jul**	**11-Jul**	**12-Jul**	**13-Jul**
	Regular Period (Kenai Opens)			**Regular Period**		
14-Jul	**15-Jul**	**16-Jul**	**17-Jul**	**18-Jul**	**19-Jul**	**20-Jul**
	Regular Period			**Regular Period**		
21-Jul	**22-Jul**	**23-Jul**	**24-Jul**	**25-Jul**	**26-Jul**	**27-Jul**
	Regular Period			**Regular Period**		
28-Jul	**29-Jul**	**30-Jul**	**31-Jul**	**1-Aug**	**2-Aug**	**3-Aug**
	Regular Period			**Regular Period**		
4-Aug	**5-Aug**	**6-Aug**	**7-Aug**	**8-Aug**	**9-Aug**	**10-Aug**
	Regular Period			**Regular Period**		
11-Aug	**12-Aug**	**13-Aug**	**14-Aug**	**15-Aug**		
	Regular Period					

Note: Up to two additional sampling dates per weeks will be added for fishery openings by emergency order.

APPENDIX C. ESSN CHINOOK SAMPLING FORM

Appendix C1.–ESSN Chinook sampling form.

ESSN Chinook Salmon Sampling Form

Date:________ Sampler(s):________________

Start Time:________ End Time: ________

Card #	Scale #	Sex	Length	Vial #	Sample location/where caught/Stat area	Age
	1					
	2					
	3					
	4					
	5					
	6					
	7					
	8					
	9					
	10					
	1					
	2					
	3					
	4					
	5					
	6					
	7					
	8					
	9					
	10					
	1					
	2					
	3					
	4					
	5					
	6					
	7					
	8					
	9					
	10					

Sex: 1-male, 2-female

Length: mid eye to fork of tail to nearest 5 mm